

1/24

	10	20	30	40	50
x	x	x	x	x	x
AAT TCC GGA GCC ATG GTG AAC GAA GCC AGA GGA AAC AGC AGC CTC AAC CCC					
TTA AGG CCT CGG TAC CAC TTG CTT CGG TCT CCT TIG TCG TCG GAG TTG GGG					
Asn Ser Gly Ala Met Val Asn Glu Ala Arg Gly Asn Ser Ser Leu Asn Pro					
	60	70	80	90	100
x	x	x	x	x	x
TGC TTG GAG GGC AGT GCC AGC AGT GGC AGT GAG AGC TCC AAA GAT AGT TCG					
ACG AAC CTC CCG TCA CCG TCG TCA CCG TCA CTC TCG AGG TTT CTA TCA AGC					
Cys Leu Glu Gly Ser Ala Ser Ser Gly Ser Glu Ser Ser Lys Asp Ser Ser					
	110	120	130	140	150
x	x	x	x	x	x
AGA TGT TCC ACC CCG GGC CTG GAC CCT GAG CGG CAT GAG AGA CTC CGG GAG					
TCT ACA AGG TGG GGC CCG GAC CTG GGA CTC GCC GTA CTC TCT GAG GCC CTC					
Arg Cys Ser Thr Pro Gly Leu Asp Pro Glu Arg His Glu Arg Leu Arg Glu					
	160	170	180	190	200
x	x	x	x	x	x
AAG ATG AGG CGG CGA TTG GAA TCT GGT GAC AAG TGG TTC TCC CTG GAA TTC					
TTC TAC TCC GCC GCT AAC CTT AGA CCA CTG TTC ACC AAG AGG GAC CTT AAG					
Lys Met Arg Arg Arg Leu Glu Ser Gly Asp Lys Trp Phe Ser Leu Glu Phe					
	210	220	230	240	250
x	x	x	x	x	x
TTC CCT CCT CGA ACT GCT GAG GGA GCT GTC AAT CTC ATC TCA AGG TTT GAC					
AAG GGA GGA GCT TGA CGA CTC CCT CGA CAG TTA GAG TAG AGT TCC AAA CTG					
Phe Pro Pro Arg Thr Ala Glu Gly Ala Val Asn Leu Ile Ser Arg Phe Asp					
	260	270	280	290	300
x	x	x	x	x	x
CGG ATG GCA GCA GGT GGC CCC CTC TAC ATA GAC GTG ACC TGG CAC CCA GCA					
GCC TAC CGT CGT CCA CCG GGG GAG ATG TAT CTG CAC TGG ACC GTG GGT CGT					
Arg Met Ala Ala Gly Gly Pro Leu Tyr Ile Asp Val Thr Trp His Pro Ala					
	310	320	330	340	350
x	x	x	x	x	x
GGT GAC CCT GGC TCA GAC AAG GAG ACC TCC TCC ATG ATG ATC GCC AGC ACC					
CCA CTG GGA CCG AGT CTG TTC CTC TGG AGG AGG TAC TAC TAG CGG TCG TGG					
Gly Asp Pro Gly Ser Asp Lys Glu Thr Ser Ser Met Met Ile Ala Ser Thr					

Fig. 1A

2/24

360	370	380	390	400
GCC	GTG	AAC	TAC	TGT
GGG	CAC	TTG	ATG	ACA
Ala	Val	Asn	Tyr	Cys
GCC	CTG	GAG	ACC	ATC
CTG	GAC	CTC	TGG	TAG
Leu	Glu	Thr	Ile	Leu
GCC	ATG	ACC	TGC	TGC
ATG	ACC	TGC	TGC	CGT
His	Met	Thr	Cys	Cys
Arg				
410	420	430	440	450
CAG	CGC	CTG	GAG	GAG
ATC	ACG	GGC	CAT	CTG
Leu	Arg	Leu	Glu	Glu
CAG	CTG	GGC	CTG	CAC
AAA	GCT	AAG	CAG	CTG
Gln	Leu	Gly	Gln	Leu
GAG	ATC	ACG	GGC	CAT
CTG	CAC	AAA	GCT	AAG
Leu	His	Lys	Ala	Lys
460	470	480	490	500
CTG	AAG	AAC	ATC	ATG
GCG	CTG	CGG	GGA	GAC
Leu	Lys	Asn	Ile	Met
CTG	AAC	TAC	GCA	GTG
GAC	CTG	GAC	CTG	GAC
Leu	Val	Asp	Leu	Val
510	520	530	540	550
CAG	TGG	GAA	GAC	CTG
CTG	GTC	ACC	CTT	CTG
Gln	Trp	Glu		
GAG	GAG	GAG	GGA	GGC
TTC	AAC	TAC	GCA	GTG
Glu	Glu	Glu	Gly	Gly
560	570	580	590	600
GAG	TGG	GAA	GAC	CTG
CTG	GTC	ACC	CTT	CTG
Gln	Trp	Glu		
AGT	GAG	TTT	GGT	GAC
TAC	TTT	GAC	ATC	TGT
Ser	Glu	Phe	Gly	Asp
610	620	630	640	650
AGT	GAG	TTT	GGT	GAC
TAC	TTT	GAC	ATC	TGT
Pro	Lys	Gly		
CAC	CCC	GAA	GCA	GGG
AGC	TTT	GAG	GCT	GAC
His	Pro	Glu	Ala	Gly
660	670	680	690	700
CAC	CCC	GAA	GCA	GGG
AGC	TTT	GAG	GCT	GAC
His	Pro	Glu	Ala	Gly
710	720	730	740	750
GTG	TCT	GCG	GGA	GCC
GAT	TTC	ATC	ATC	ACG
Val	Ser	Ala	Gly	Ala
GTG	GGG	CTT	CGT	CCC
TGC	AAA	CTC	CGA	CTG
Val	Ser	Ala	Gly	Ala
760	770	780	790	800
GTG	TCT	GCG	GGA	GCC
GAT	TTC	ATC	ATC	ACG
Val	Ser	Ala	Gly	Ala
GTG	GGG	CTT	CGT	CCC
TGC	AAA	CTC	CGA	CTG
Val	Ser	Ala	Gly	Ala

Fig. 1B

3/24

720 730 740 750 760
 * * * * *
 ACA TTC TTC CGC TTT GTG AAG GCA TGC ACC GAC ATG GGC ATC ACT TGC CCC
 TGT AAG AAG GCG AAA CAC TTC CGT ACG TGG CTG TAC CCG TAG TGA ACG GGG
 Thr Phe Phe Arg Phe Val Lys Ala Cys Thr Asp Met Gly Ile Thr Cys Pro

770 780 790 800 810
 * * * * *
 ATC GTC CCC GGG ATC TTT CCC ATC CAG GGC TAC CAC TCC CTT CGG CAG CTT
 TAG CAG GGG CCC TAG AAA GGG TAG GTC CCG ATG GTG AGG GAA GCC GTC GAA
 Ile Val Pro Gly Ile Phe Pro Ile Gln Gly Tyr His Ser Leu Arg Gln Leu

820 830 840 850 860
 * * * * *
 GTG AAG CTG TCC AAG CTG GAG GTG CCA CAG GAG ATC AAG GAC GTG ATT GAG
 CAC TTC GAC AGG TTC GAC CTC CAC GGT GTC CTC TAG TTC CTG CAC TAA CTC
 Val Lys Leu Ser Lys Leu Glu Val Pro Gln Glu Ile Lys Asp Val Ile Glu

870 880 890 900 910
 * * * * *
 CCA ATC AAA GAC AAC GAT GCT GCC ATC CGC AAC TAT GGC ATC GAG CTG GCC
 GGT TAG TTT CTG TTG CTA CGA CCG TAG GCG TTG ATA CCG TAG CTC GAC CCG
 Pro Ile Lys Asp Asn Asp Ala Ala Ile Arg Asn Tyr Gly Ile Glu Leu Ala

920 930 940 950 960
 * * * * *
 GTG AGC CTG TGC CAG GAG CTT CTG GCC AGT GGC TTG GTG CCA GGC CTC CAC
 CAC TCG GAC ACG GTC CTC GAA GAC CCG TCA CCG AAC CAC GGT CCG GAG GTG
 Val Ser Leu Cys Gln Glu Leu Leu Ala Ser Gly Leu Val Pro Gly Leu His

970 980 990 1000 1010 1020
 * * * * * *
 TTC TAC ACC CTC AAC CGC GAG ATG GCT ACC ACA GAG GTG CTG AAG CGC CTG
 AAG ATG TGG GAG TTG GCG CTC TAC CGA TGG TGT CTC CAC GAC TTC GCG GAC
 Phe Tyr Thr Leu Asn Arg Glu Met Ala Thr Thr Glu Val Leu Lys Arg Leu

1030 1040 1050 1060 1070
 * * * * *
 GGG ATG TGG ACT GAG GAC CCC AGG CGT CCC CTA CCC TGG GCT CTC AGT GCC
 CCC TAC ACC TGA CTC CTG GGG TCC GCA GGG GAT GGG ACC CGA GAG TCA CCG
 Gly Met Trp Thr Glu Asp Pro Arg Arg Pro Leu Pro Trp Ala Leu Ser Ala

Fig. 1C

4/24

1080	1090	1100	1110	1120
x	x	x	x	x
CAC CCC AAG CGC CGA GAG GAA GAT GTA CGT CCC ATC TTC TGG GCC TCC AGA				
GTG GGG TTC GCG GCT CTC CTT CTA CAT GCA GGG TAG AAG ACC CGG AGG TCT				
His Pro Lys Arg Arg Glu Glu Asp Val Arg Pro Ile Phe Trp Ala Ser Arg				

1130	1140	1150	1160	1170
x	x	x	x	x
CCA AAG AGT TAC ATC TAC CGT ACC CAG GAG TGG GAC GAG TTC CCT AAC GGC				
GGT TTC TCA ATG TAG ATG GCA TGG GTC CTC ACC CTG CTC AAG GGA TIG CCG				
Pro Lys Ser Tyr Ile Tyr Arg Thr Gln Glu Trp Asp Glu Phe Pro Asn Gly				

1180	1190	1200	1210	1220
x	x	x	x	x
CGC TGG GGC AAT TCC TCT TCC CCT GCC TTT GGG GAG CTG AAG GAC TAC TAC				
GCG ACC CCG TTA AGG AGA AGG GGA CGG AAA CCC CTC GAC TTC CTG ATG ATG				
Arg Trp Gly Asn Ser Ser Ser Pro Ala Phe Gly Glu Leu Lys Asp Tyr Tyr				

1230	1240	1250	1260	1270
x	x	x	x	x
CTC TTC TAC CTG AAG AGC AAG TCC CCC AAG GAG GAG CTG CTG AAG ATG TGG				
GAG AAG ATG GAC TTC TCG TTC AGG GGG TTC CTC CTC GAC GAC TTC TAC ACC				
Leu Phe Tyr Leu Lys Ser Lys Ser Pro Lys Glu Glu Leu Leu Lys Met Trp				

1280	1290	1300	1310	1320
x	x	x	x	x
GGG GAG GAG CTG ACC AGT GAA GCA AGT GTC TTT GAA GTC TTT GTT CTT TAC				
CCC CTC CTC GAC TGG TCA CTT CGT TCA CAG AAA CTT CAG AAA CAA GAA ATG				
Gly Glu Glu Leu Thr Ser Glu Ala Ser Val Phe Glu Val Phe Val Leu Tyr				

1330	1340	1350	1360	1370
x	x	x	x	x
CTC TCG GGA GAA CCA AAC CGG AAT GGT CAC AAA GTG ACT TGC CTG CCC TGG				
GAG AGC CCT CTT GGT TTG GCC TTA CCA GTG TTT CAC TGA ACG GAC GGG ACC				
Leu Ser Gly Glu Pro Asn Arg Asn Gly His Lys Val Thr Cys Leu Pro Trp				

1380	1390	1400	1410	1420
x	x	x	x	x
AAC GAT GAG CCC CTG GCG GCT GAG ACC AGC CTG CTG AAG GAG GAG CTG CTG				
TTG CTA CTC GGG GAC CGC CGA CTC TGG TCG GAC GAC TTC CTC CTC GAC GAC				
Asn Asp Glu Pro Leu Ala Ala Glu Thr Ser Leu Leu Lys Glu Glu Leu Leu				

Fig. 1D

5/24

1430	1440	1450	1460	1470	
* CGG GTG AAC CGC CAG GGC ATC CTC ACC ATC AAC TCA CAG CCC AAC ATC AAC	* GCG GTC CCG TAG GAG TGG TAG TTG AGT GTC GGG TTG TAG TTG	* Arg Val Asn Arg Gln Gly Ile Leu Thr Ile Asn Ser Gln Pro Asn Ile Asn			
1480	1490	1500	1510	1520	1530
* GGG AAG CCG TCC TCC GAC CCC ATC GTG GGC TGG GGC CCC AGC GGG GGC TAT	* CCC TTC GGC AGG AGG CTG GGG TAG CAC CCG ACC CCG GGG TCG CCC CCG ATA	* Gly Lys Pro Ser Ser Asp Pro Ile Val Gly Trp Gly Pro Ser Gly Gly Tyr			
	1540	1550	1560	1570	1580
	* GTC TTC CAG AAG GCC TAC TTA GAG TTT TTC ACT TCC CGC GAG ACA GCG GAA	* CAG AAG GTC TTC CCG ATG AAT CTC AAA AAG TGA AGG GCG CTC TGT CCG CTT	* Val Phe Gln Lys Ala Tyr Leu Glu Phe Phe Thr Ser Arg Glu Thr Ala Glu		
	1590	1600	1610	1620	1630
	* GCA CTT CTG CAA GTG CTG AAG AAG TAC GAG CTC CGG GTT AAT TAC CAC CTT	* CGT GAA GAC GTT CAC GAC TTC TTC ATG CTC GAG GCC CAA TTA ATG GTG GAA	* Ala Leu Leu Gln Val Leu Lys Lys Tyr Glu Leu Arg Val Asn Tyr His Leu		
	1640	1650	1660	1670	1680
	* GTC AAT GTG AAG GGT GAA AAC ATC ACC AAT GCC CCT GAA CTG CAG CCG AAT	* CAG TTA CAC TTC CCA CTT TTG TAG TGG TTA CGG GGA CTT GAC GTC GGC TTA	* Val Asn Val Lys Gly Glu Asn Ile Thr Asn Ala Pro Glu Leu Gln Pro Asn		
	1690	1700	1710	1720	1730
	* GCT GTC ACT TGG GGC ATC TTC CCT GGG CGA GAG ATC ATC CAG CCC ACC GTA	* CGA CAG TGA ACC CCG TAG AAG GGA CCC GCT CTC TAG TAG GTC GGG TGG CAT	* Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Ile Gln Pro Thr Val		
	1740	1750	1760	1770	1780
	* GTG GAT CCC GTC AGC TTC ATG TTC TGG AAG GAC GAG GCC TTT GCC CTG TGG	* CAC CTA GGG CAG TCG AAG TAC AAG ACC TTC CTG CTC CGG AAA CCG GAC ACC	* Val Asp Pro Val Ser Phe Met Phe Trp Lys Asp Glu Ala Phe Ala Leu Trp		

Fig. 1E

6/24

1790	1800	1810	1820	1830	
ATT GAG CGG TGG GGA AAG CTG TAT GAG GAG GAG TCC CCG TCC CGC ACC ATC					
TAA CTC GCC ACC CCT TTC GAC ATA CTC CTC CTC AGG GGC AGG GCG TGG TAG					
Ile Glu Arg Trp Gly Lys Leu Tyr Glu Glu Glu Ser Pro Ser Arg Thr Ile					
1840	1850	1860	1870	1880	
ATC CAG TAC ATC CAC GAC AAC TAC TTC CTG GTC AAC CTG GTG GAC AAT GAC					
TAG GTC ATG TAG GTG CTG TTG ATG AAG GAC CAG TTG GAC CAC CTG TTA CTG					
Ile Gln Tyr Ile His Asp Asn Tyr Phe Leu Val Asn Leu Val Asp Asn Asp					
1890	1900	1910	1920	1930	
TTC CCA CTG GAC AAC TGC CTC TGG CAG GTG GTG GAA GAC ACA TTG GAG CTT					
AAG GGT GAC CTG TTG ACG GAG ACC GTC CAC CAC CTT CTG TGT AAC CTC GAA					
Phe Pro Leu Asp Asn Cys Leu Trp Gln Val Val Glu Asp Thr Leu Glu Leu					
1940	1950	1960	1970	1980	1990
CTC AAC AGG CCC ACC CAG AAT GCG AGA GAA ACG GAG GGT CCA TGACCCCTGCG					
GAG TTG TCC GGG TGG GTC TTA CGC TCT CTT TGC CTC CGA GGT ACTGGGACGC					
Leu Asn Arg Pro Thr Gln Asn Ala Arg Glu Thr Glu Ala Pro					
2000	2010	2020	2030	2040	2050
TCCTGACGCC CTGCGTTGGA GCCACTCCTG TCCCGCCTTC CTCCTCCACA GTGCTGCTTC					
AGGACTGCGG GACGCAACCT CCGTGAGGAC AGGGCGGAAG GAGGAGGTGT CACGACGAAG					
2060	2070	2080	2090	2100	2110
TCTTGGGAAC TCCACTCTCC TTCGTGTCTC TCCCACCCCG GCCTCCACTC CCCCACCTGA					
AGAACCTTGG AGGTGAGAGG AAGCACAGAG AGGGTGGGGC CGGAGGTGAG GGGGTGGACT					
2120	2130	2140	2150	2160	2170
CAATGGCAGC TAGACTGGAG TGAGGCTTCC AGGCTCTTCC TGGACCTGAG TCGGCCCCAC					
GTTACCGTGC ATCTGACCTC ACTCCGAAGG TCCGAGAAGG ACCTGGACTC AGCCGGGGTG					
2180	2190	2200	2210	2220	
ATGGGAACCT AGTACTCTCT GTCTTAAAAA AAAAAAAAAA AAAGGAATTC					
TACCCCTTGA TCATGAGAGA CGAGATTTTT TTTTTTTTTT TTTCTTAAG					

Fig. 1F

AMVNE ARGNS SLNPC LEGSA SSGSE SSKDS SRCST PGLDP ERHER LREKM RRRLE S--GDKW ESLEF mthfr
 ms fFHAs qRdal nqSLa evqGqin vSFEF ecometf
 ms fFHAn qREal nqSLa evqGqin vSFEF stymetf
 ms iRdLy haraspf iSLEF ysRADI

100.
 FPPRT AEGAV NLISR FDRMA AGGPL YIDVT WHPAG DPGSD KETSS MMIA S TAVNY CGLET ILHMT mthfr
 FPPRT sEmeq tLwns iDRIs sIkPk fvsVT y--ga nsGer drThs i-lkg ik-dr tGLEa aphIT ecometf
 FPPRT sEmeq tLwns iDRIs sIkPk fvsVT y--ga nsGer drThs v-lkg ik-er tGLEa aphIT stymetf
 FPPKT eGtr NLmeR mHRMt AlDPL fItVT W--ga -ggtt aEktI t-lAS lAqqt lniPv cmHIT ysRADI

200.
 CCRQR LEEIT GHLHK AKQLG LKNIM ALRGD -PIGDQ WEEEE GGFNY AVGLV KHIRS EFGDY FDICV mthfr
 Cidat pdElr tiard ywnng irhIv ALRGD lPpGsg kPE-- ---mY AsdLV tlik- EvaD- FDIsV ecometf
 Cidat rdElr tiard ywnng irhIv ALRGD lPpGsg kPE-- ---mY AadLV glik- EvaD- FDIsV stymetf
 CtnTe kaild daLdr cynaG irNI l ALRGn lPIGvv WlvSq snrll nmrLf> ysRADI

300.
 AGYPK GHPEA GSFEA DLKHL KEKVS AGADF IITQL FFEAD TFFRF VKACT DMGIT CPIVP GIFPI mthfr
 AaYPE vHPEA kSaQA DLInL KrKVd AGAnr aITQF FFdve syl RF rdrCv saGld velIP GIIPv ecometf
 AaYPE vHPEA kSaQA DLInL KrKVd AGAnr aITQF FFdve syl RF rdrCv saGld velIP GIIPv stymetf

400.
 QGYHS LRQLV KLSKL EVPQE IKDVI EPIKD NDAAI RN-YGI ELAVS LCQEL LASGL VPGLH FYTLN mthfr
 snfkq akkfa dmtnv rIPaw maqmf dgl-D dDAet RklvGa niAmd mvkiL sreg- VkdFH FYTLN ecometf
 snfkq akkfa dmtnv rIPsw mslmf Egl-D nDAet RklvGa niAmd mvkiL sreg- VkdFH FYTLN stymetf

R-EMAT TEVLK RLGMW TEDPR RPLPW ALSAH PKRRE EDVRP IFWAS RPKSY IYRTO EWDEF PNGRW mthfr
 RaEMsy a-ich tLGvr pgl> ecometf
 RaEMsy a-ich tLGvr pgl> stymetf

GNSSS PAFGE LKDYD LFYLK SKSPK E mthfr

Fig. 2

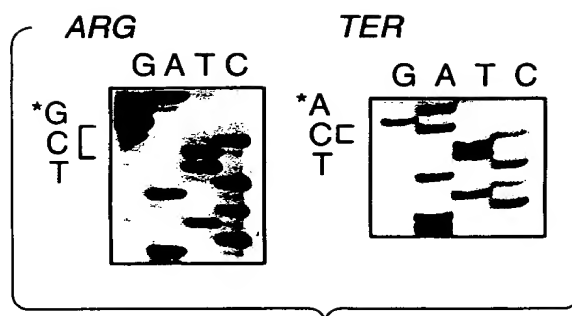


Fig. 3A

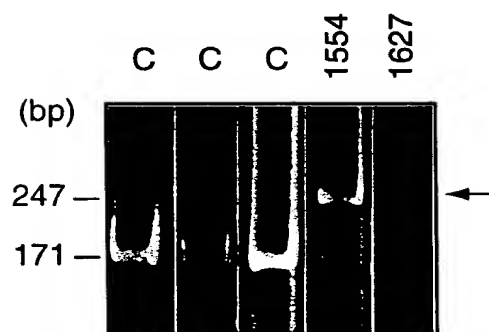


Fig. 3B

9/24

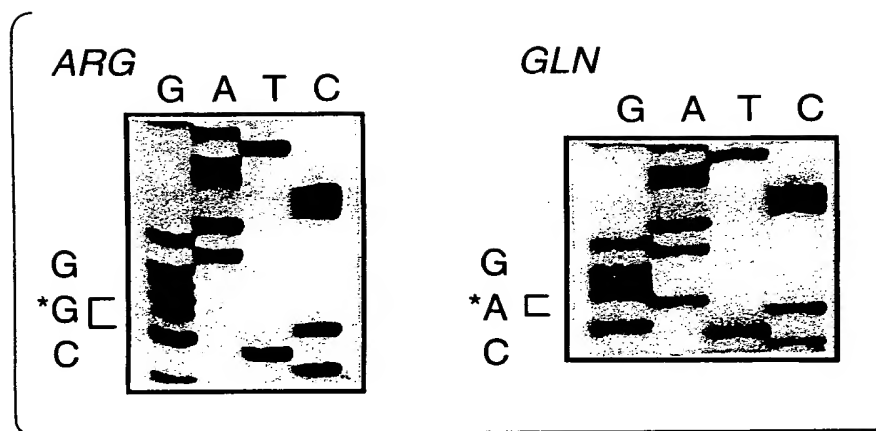


Fig. 4A

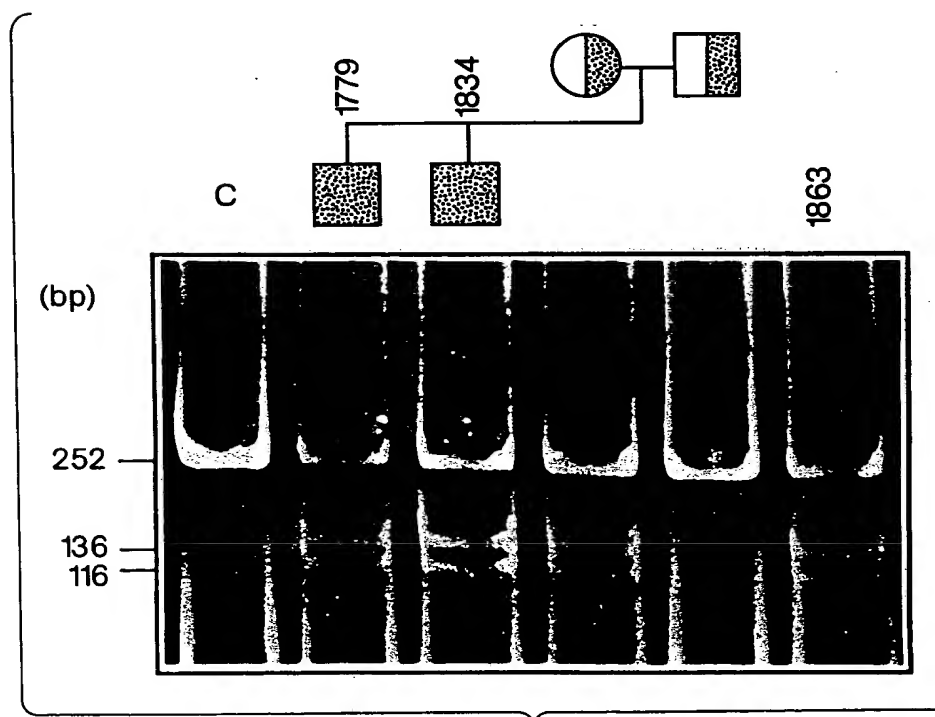


Fig. 4B

10/24

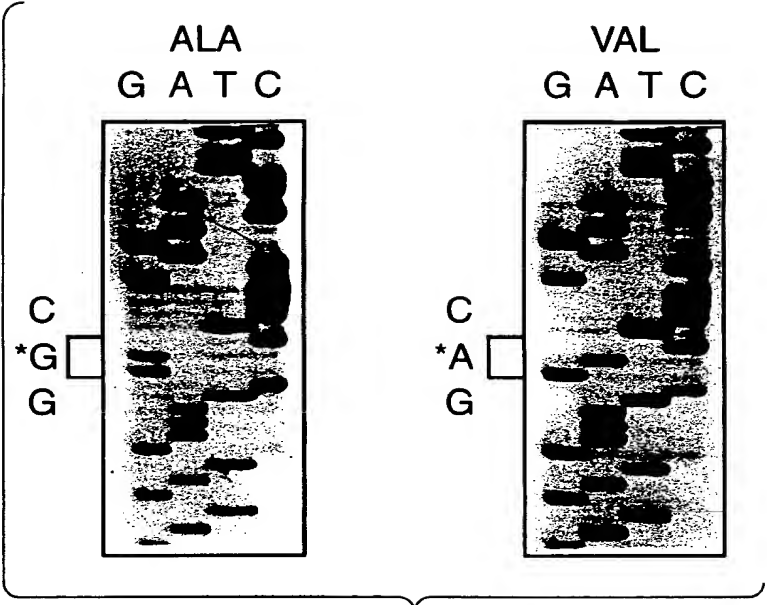


Fig. 5A

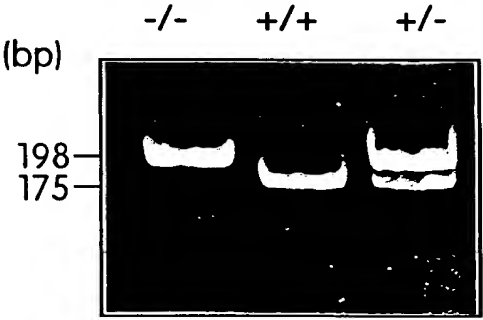


Fig. 5B

11/24

AAI	TCC	GGA	GCC	ATG	GTG	AAC	GAA	GCC	AGA	GGA	AAC	AGC	AGC	CTC	AAC	CCC	TGC	TTG	GAG	60
				Met	Val	Asn	Glu	Ala	Arg	Gly	Asn	Ser	Ser	Leu	Asn	Pro	Cys	Leu	Glu	16
GGC	AGT	GCC	AGC	AGT	GGC	AGT	GAG	AGC	TCC	AAA	GAT	AGT	TCG	AGA	TGT	TCC	ACC	CCG	GGC	120
Gly	Ser	Ala	Ser	Ser	Gly	Ser	Glu	Ser	Ser	Lys	Asp	Ser	Ser	Arg	Cys	Ser	Thr	Pro	Gly	36
CTG	GAC	CCT	GAG	CGG	CAT	GAG	AGA	CTC	CGG	GAG	AAG	ATG	AGG	CGG	CGA	TTG	GAA	TCT	GGT	180
Leu	Asp	Pro	Glu	Arg	His	Glu	Arg	Leu	Arg	Glu	Lys	Met	Arg	Arg	Arg	Leu	Glu	Ser	Gly	56
GAC	AAG	TGG	TTC	TCC	CTG	GAA	TTC	TTC	CCT	CCT	CGA	ACT	GCT	GAG	GGA	GCT	GTC	AAT	CTC	240
Asp	Lys	Trp	Phe	Ser	Leu	Glu	Phe	Phe	Pro	Pro	Arg	Thr	Ala	Glu	Gly	Ala	Val	Asn	Leu	76
ATC	TCA	AGG	TTT	GAC	CGG	ATG	GCA	GCA	GGT	GGC	CCC	CTC	TAC	ATA	GAC	GTG	ACC	TGG	CAC	300
Ile	Ser	Arg	Phe	Asp	Arg	Met	Ala	Ala	Gly	Gly	Pro	Leu	Tyr	Ile	Asp	Val	Thr	Trp	His	96
CCA	GCA	GGT	GAC	CCT	GGC	TCA	GAC	AAG	GAG	ACC	TCC	TCC	ATG	ATG	ATC	GCC	AGC	ACC	GCC	360
Pro	Ala	Gly	Asp	Pro	Gly	Ser	Asp	Lys	Glu	Thr	Ser	Ser	Met	Met	Ile	Ala	Ser	Thr	Ala	116
GTG	AAC	TAC	TGT	GGC	CTG	GAG	ACC	ATC	CTG	CAC	ATG	ACC	TGC	TGC	CGT	CAG	CGC	CTG	GAG	420
Val	Asn	Tyr	Cys	Gly	Leu	Glu	Thr	Ile	Leu	His	Met	Thr	Cys	Cys	Arg	Gln	Arg	Leu	Glu	136
GAG	ATC	ACG	GGC	CAT	CTG	CAC	AAA	GCT	AAG	CAG	CTG	GGC	CTG	AAG	AAC	ATC	ATG	GCG	CTG	480
Glu	Ile	Thr	Gly	His	Leu	His	Lys	Ala	Lys	Gln	Leu	Gly	Leu	Lys	Asn	Ile	Met	Ala	Leu	156
CGG	GGA	GAC	CCA	ATA	GGT	GAC	CAG	TGG	GAA	GAG	GAG	GAG	GGA	GGC	TTC	AAC	TAC	GCA	GTG	540
Arg	Gly	Asp	Pro	Ile	Gly	Asp	Gln	Trp	Glu	Glu	Glu	Glu	Gly	Gly	Phe	Asn	Tyr	Ala	Val	176
GAC	CTG	GTG	AAG	CAC	ATC	CGA	AGT	GAG	TTT	GGT	GAC	TAC	TTT	GAC	ATC	TGT	GTG	GCA	GGT	600
Asp	Leu	Val	Lys	His	Ile	Arg	Ser	Glu	Phe	Gly	Asp	Tyr	Phe	Asp	Ile	Cys	Val	Ala	Gly	196
TAC	CCC	AAA	GGC	CAC	CCC	GAA	GCA	GGG	AGC	TTT	GAG	GCT	GAC	CTG	AAG	CAC	TTG	AAG	GAG	660
Tyr	Pro	Lys	Gly	His	Pro	Glu	Ala	Gly	Ser	Phe	Glu	Ala	Asp	Leu	Lys	His	Leu	Lys	Glu	216
AAG	GTG	TCT	GCG	GGA	GCC	GAT	TTC	ATC	ATC	ACG	CAG	CTT	TTC	TTT	GAG	GCT	GAC	ACA	TTC	720
Lys	Val	Ser	Ala	Gly	Ala	Asp	Phe	Ile	Ile	Thr	Gln	Leu	Phe	Phe	Glu	Ala	Asp	Thr	Phe	236

Fig. 6A

12/24

TTC	CGC	TTT	GTG	AAG	GCA	TGC	ACC	GAC	ATG	GGC	ATC	ACT	TGC	CCC	ATC	GTC	CCC	GGG	ATC	780
Phe	Arg	Phe	Val	Lys	Ala	Cys	Thr	Asp	Met	Gly	Ile	Thr	Cys	Pro	Ile	Val	Pro	Gly	Ile	256
TTT	CCC	ATC	CAG	GGC	TAC	CAC	TCC	CTT	CGG	CAG	CTT	GTG	AAG	CTG	TCC	AAG	CTG	GAG	GTG	840
Phe	Pro	Ile	Gln	Gly	Tyr	His	Ser	Leu	Arg	Gln	Leu	Val	Lys	Leu	Ser	Lys	Leu	Glu	Val	276
CCA	CAG	GAG	ATC	AAG	GAC	GTG	ATT	GAG	CCA	ATC	AAA	GAC	AAC	GAT	GCT	GCC	ATC	CGC	AAC	900
Pro	Gln	Glu	Ile	Lys	Asp	Val	Ile	Glu	Pro	Ile	Lys	Asp	Asn	Asp	Ala	Ala	Ile	Arg	Asn	296
TAT	GGC	ATC	GAG	CTG	GCC	GTG	AGC	CTG	TGC	CAG	GAG	CTT	CTG	GCC	AGT	GGC	TTG	GTG	CCA	960
Tyr	Gly	Ile	Glu	Leu	Ala	Val	Ser	Leu	Cys	Gln	Glu	Leu	Leu	Ala	Ser	Gly	Leu	Val	Pro	316
GGC	CTC	CAC	TTC	TAC	ACC	CTC	AAC	CGC	GAG	ATG	GCT	ACC	ACA	GAG	GTG	CTG	AAG	CGC	CTG	1020
Gly	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Glu	Met	Ala	Thr	Thr	Glu	Val	Leu	Lys	Arg	Leu	336
GGG	ATG	TGG	ACT	GAG	GAC	CCC	AGG	CGT	CCC	CTA	CCC	TGG	GCT	CTC	AGT	GCC	CAC	CCC	AAG	1080
Gly	Met	Trp	Thr	Glu	Asp	Pro	Arg	Arg	Pro	Leu	Pro	Trp	Ala	Leu	Ser	Ala	His	Pro	Lys	356
CGC	CGA	GAG	GAA	GAT	GTA	CGT	CCC	ATC	TTC	TGG	GCC	TCC	AGA	CCA	AAG	AGT	TAC	ATC	TAC	1140
Arg	Arg	Glu	Glu	Asp	Val	Arg	Pro	Ile	Phe	Trp	Ala	Ser	Arg	Pro	Lys	Ser	Tyr	Ile	Tyr	376
CGT	ACC	CAG	GAG	TGG	GAC	GAG	TTC	CCT	AAC	GGC	CGC	TGG	GGC	AAT	TCC	TCT	TCC	CCT	GCC	1200
Arg	Thr	Gln	Glu	Trp	Asp	Glu	Phe	Pro	Asn	Gly	Arg	Trp	Gly	Asn	Ser	Ser	Ser	Pro	Ala	396
TTT	GGG	GAG	CTG	AAG	GAC	TAC	TAC	CTC	TTC	TAC	CTG	AAG	AGC	AAG	TCC	CCC	AAG	GAG	GAG	1260
Phe	Gly	Glu	Leu	Lys	Asp	Tyr	Tyr	Leu	Phe	Tyr	Leu	Lys	Ser	Lys	Ser	Pro	Lys	Glu	Glu	416
CTG	CTG	AAG	ATG	TGG	GGG	GAG	GAG	CTG	ACC	AGT	GAA	GCA	AGT	GTC	TTT	GAA	GTC	TTT	GTT	1320
Leu	Leu	Lys	Met	Trp	Gly	Glu	Glu	Leu	Thr	Ser	Glu	Ala	Ser	Val	Phe	Glu	Val	Phe	Val	436
CTT	TAC	CTC	TGG	GGA	GAA	CCA	AAC	CGG	AAT	GGT	CAC	AAA	GTG	ACT	TGC	CTG	CCC	TGG	AAC	1380
Leu	Tyr	Leu	Ser	Gly	Glu	Pro	Asn	Arg	Asn	Gly	His	Lys	Val	Thr	Cys	Leu	Pro	Trp	Asn	456
GAT	GAG	CCC	CTG	GCG	GCT	GAG	ACC	AGC	CTG	CTG	AAG	GAG	GAG	CTG	CTG	CGG	GTG	AAC	CGC	1440
Asp	Glu	Pro	Leu	Ala	Ala	Glu	Thr	Ser	Leu	Leu	Lys	Glu	Glu	Leu	Leu	Arg	Val	Asn	Arg	476

Fig. 6B

CAG GGC ATC CTC ACC ATC AAC TCA CAG CCC AAC ATC AAC GGG AAG CCG TCC TCC GAC CCC 1500
 Gln Gly Ile Leu Thr Ile Asn Ser Gln Pro Asn Ile Asn Gly Lys Pro Ser Ser Asp Pro 496
 ATC GTG GGC TGG GGC CCC AGC GGG GGC TAT GTC TTC CAG AAG GCC TAC TTA GAG TTT TTC 1560
 Ile Val Gly Trp Gly Pro Ser Gly Gly Tyr Val Phe Gln Lys Ala Tyr Leu Glu Phe Phe 516
 ACT TCC CGC GAG ACA GCG GAA GCA CTT CTG CAA GTG CTG AAG AAG TAC GAG CTC CGG GTT 1620
 Thr Ser Arg Glu Thr Ala Glu Ala Leu Leu Gln Val Leu Lys Lys Tyr Glu Leu Arg Val 536
 AAT TAC CAC CTT GTC AAT GTG AAG GGT GAA AAC ATC ACC AAT GCC CCT GAA CTG CAG CCG 1680
 Asn Tyr His Leu Val Asn Val Lys Gly Glu Asn Ile Thr Asn Ala Pro Glu Leu Gln Pro 556
 AAT GCT GTC ACT TGG GGC ATC TTC CCT GGG CGA GAG ATC ATC CAG CCC ACC GTA GTG GAT 1740
 Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Ile Gln Pro Thr Val Val Asp 576
 CCC GTC AGC TTC ATG TTC TGG AAG GAC GAG GCC TTT GCC CTG TGG ATT GAG CGG TGG GGA 1800
 Pro Val Ser Phe Met Phe Trp Lys Asp Glu Ala Phe Ala Leu Trp Ile Glu Arg Trp Gly 596
 AAG CTG TAT GAG GAG GAG TCC CCG TCC CGC ACC ATC ATC CAG TAC ATC CAC GAC AAC TAC 1860
 Lys Leu Tyr Glu Glu Glu Ser Pro Ser Arg Thr Ile Ile Gln Tyr Ile His Asp Asn Tyr 616
 TTC CTG GTC AAC CTG GTG GAC AAT GAC TTC CCA CTG GAC AAC TGC CTC TGG CAG GTG GTG 1920
 Phe Leu Val Asn Leu Val Asp Asn Asp Phe Pro Leu Asp Asn Cys Leu Trp Gln Val Val 636
 GAA GAC ACA TTG GAG CTT CTC AAC AGG CCC ACC CAG AAT GCG AGA GAA ACG GAG GCT CCA 1980
 Glu Asp Thr Leu Glu Leu Leu Asn Arg Pro Thr Gln Asn Ala Arg Glu Thr Glu Ala Pro 656
 TGA CCC TGC GTC CTG ACG CCC TGC GTT GGA GCC ACT CCT GTC CCG CCT TCC TCC TCC ACA 2040
 End
 GTG CTG CTT CTC TTG GGA ACT CCA CTC TCC TTC GTG TCT CTC CCA CCC CGG CCT CCA CTC 2100
 CCC CAC CTG ACA ATG GCA GCT AGA CTG GAG TGA GGC TTC CAG GCT CTT CCT GGA CCT GAG 2160
 TCG GCC CCA CAT GGG AAC CTA GTA CTC TCT GCT CTA AAA AAA AAA AAA AAA AAG GAA TT 2220

Fig. 6C

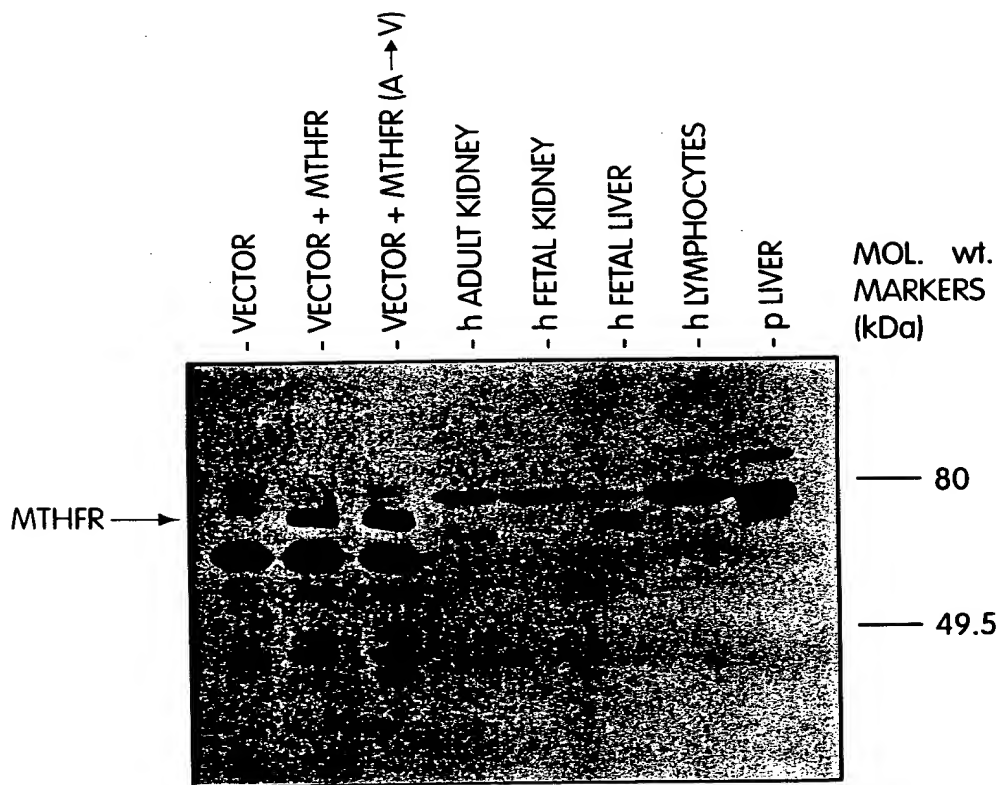


Fig. 7A

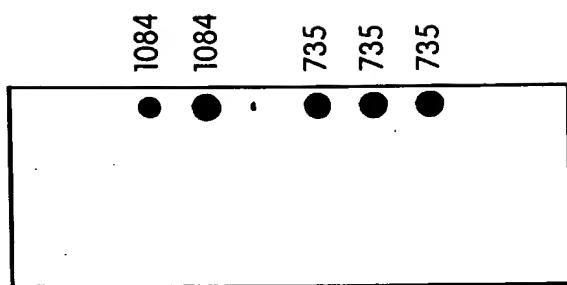


Fig. 10A

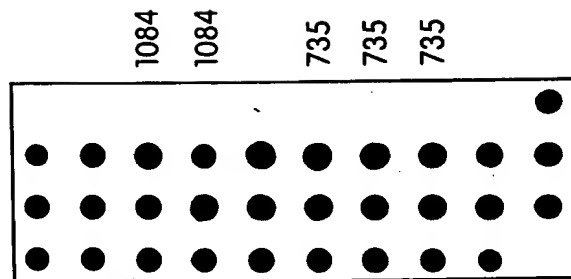


Fig. 10B

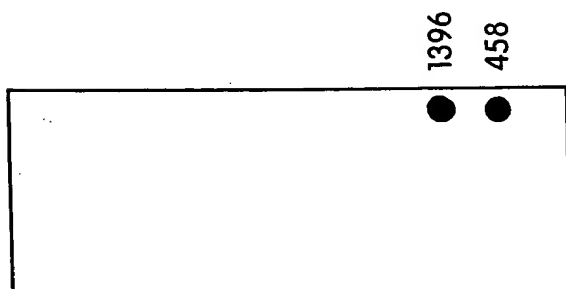


Fig. 10C

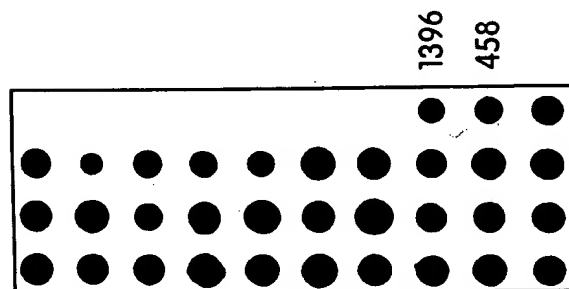


Fig. 10D

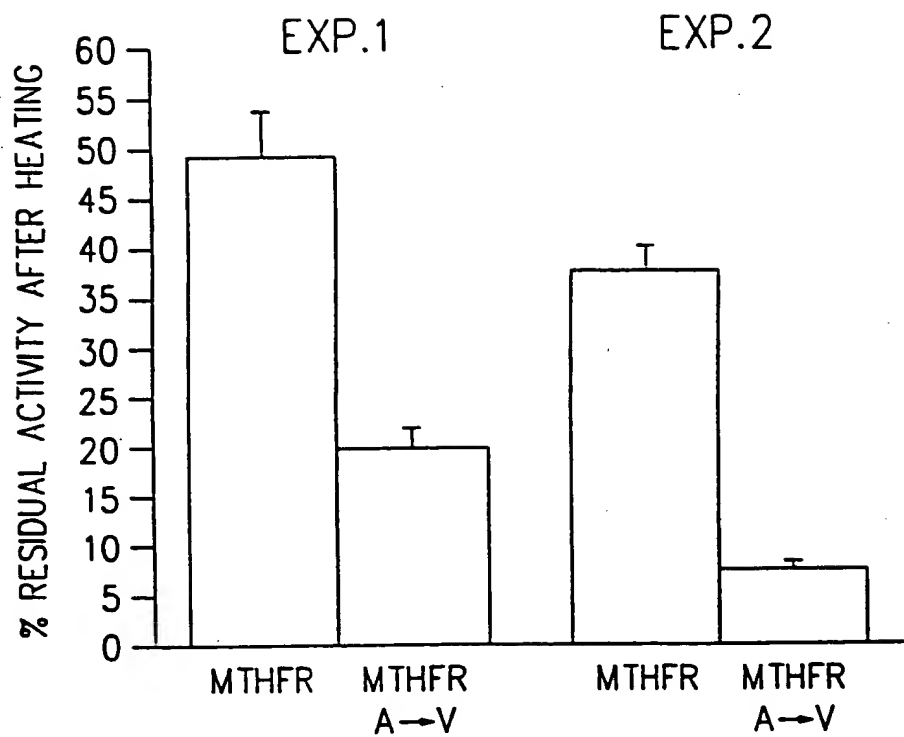


Fig. 7B

MTHFR: KHLKEKVSAGADF I I TQLFFEADTFFR
 DHFR: GHLKLFVT----R-IMQD-FESDTFFP

Fig. 11

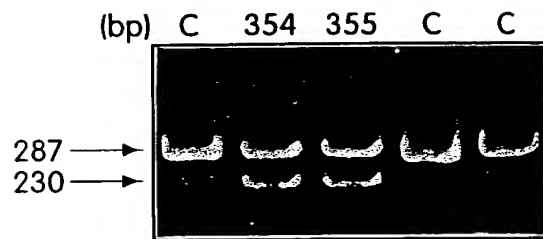


Fig. 8A

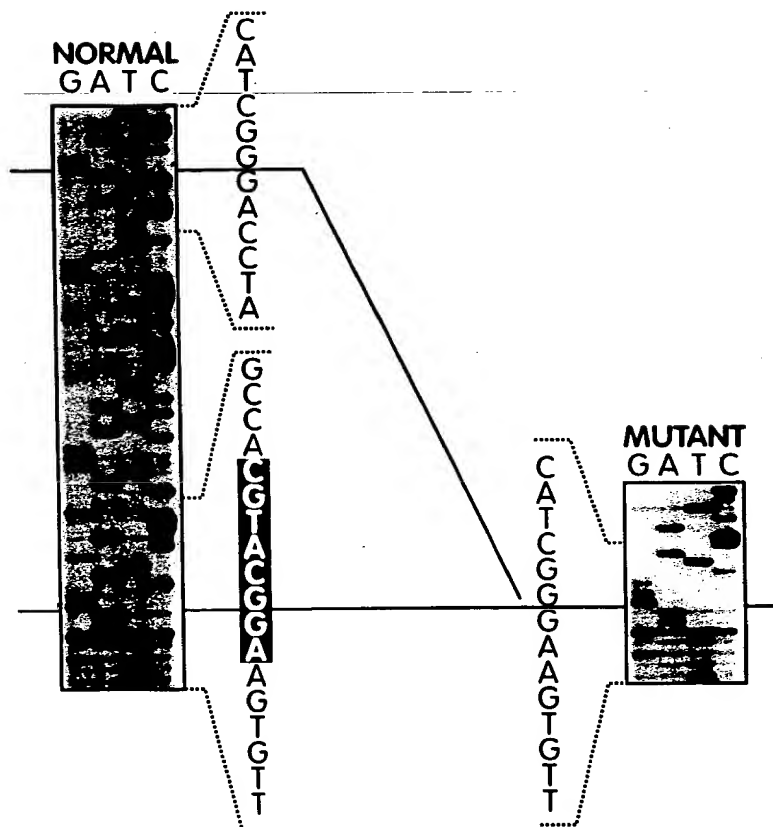


Fig. 8B

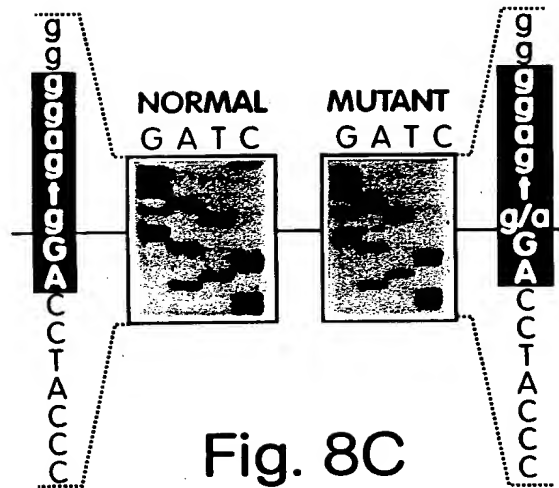


Fig. 8C

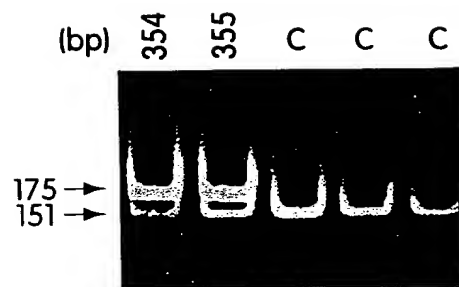


Fig. 8D

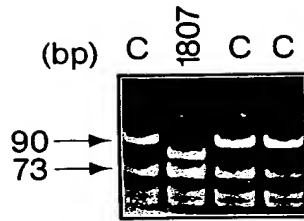


Fig. 9A

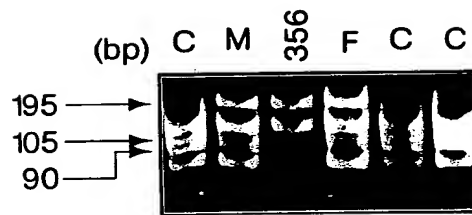


Fig. 9B

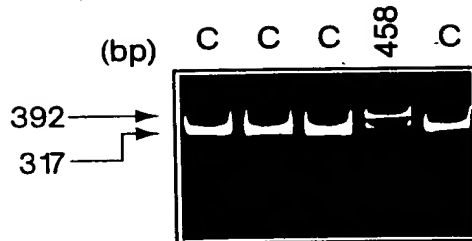


Fig. 9C

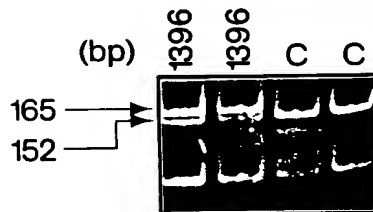


Fig. 9D

19/24

EXON 1: 246 bp (bp 3-248)

*

gggtgtggct gcctgcccc tgatgctccc tgccccaccc tgtgcagtag **GAACCCAGCC**
ATGGTGAACG AAGCCAGAGG AAACAGCAGC CTCAACCCCT GCTTGGAGGG CAGTGCCAGC
 AGTGGCAGTG AGAGCTCCAA AGATAGTTCG AGATGTTCCA CCCCGGGCCT GGACCCTGAG
 CGGCATGAGA GACTCCGGA GAAGATGAGG CGGCGATTGG AATCTGGTGA CAAGTGGTTC
 TCCCTGGAAT TCTTCCCTCC TCGAACTGCT GAGGGAGCTG TCAATCTCAT CTCAAG^gtaa
 actcatgcaa ggtaaggtg agaggcgga gtggtggtgc ctgggg

EXON 2: 239 bp (bp 249-487)

acggatgg tattttctctt ggaacctctc ttcagaaaca aacccccctacag **GTTTGACCGG**
ATGGCAGCAG GTGGCCCCCT CTACATAGAC GTGACCTGGC ACCCAGCAGG TGACCCTGGC
 TCAGACAAGG AGACCTCCTC CATGATGATC GCCAGCACCG CCGTGAAC^TA CTGTGGCCTG
 GAGACCATCC TGCACATGAC CTGCTGCCGT CAGCGCCTGG AGGAGATCAC GGGCCATCTG
 CACAAAGCTA AGCAGCTGGG CCTGAAGAAC ATCATGGCGC TCGGGGGAG^g t^ggtggagcca
 gcactcccc acactctggg ttctggcttt cccggaggc

EXON 3: 111 bp (bp 488-598)

tctggagggtt ggggtgagacc cagtgactat gacctccacc aaccttg^cag **ACCCAATAGG**
TGACCAGTGG GAAGAGGAGG AGGGAGGCTT CAACTACGCA GTGGACCTGG **TGAAGCACAT**
CCGAAGTGAG TTTGGTGACT ACTTTGACAT CTGTGTGGCA ^Ggtgagtggc tggatcatcc
 tggtggcggg gatggagcta gggaggctga

EXON 4: 194 bp (bp 599-792)

ccttgaacag gtggaggcca gcctctcctg actgtcatcc ctattggcag **GTTACCCCAA**
AGGCCACCCC GAAGCAGGGA GCTTTGAGGC TGACCTGAAG CACTTGAAGG **AGAAGGTGTC**
TGCGGGAGCC GATTTTCATCA TCACGCAGCT TTTCTTTGAG GCTGACACAT **TCTTCCGCTT**
TGTGAAGGCA TGCACCGACA TGGGCATCAC TTGCCCCATC GTCCCCGGGA **TCTTTCCCAT**
CCAG^gtgagg ggcccaggag agcccataag ctccctccac cccactctca ccgc

EXON 5: 251 bp (bp 793-1043)

gctggccagc agccgccaca gcccctcatg tcttggacag **GGCTACCACT** **CCCTTCGGCA**
GCTTGTGAAG CTGTCCAAGC TGGAGGTGCC ACAGGAGATC AAGGACGTGA **TTGAGCCAAT**
CAAAGACAAC GATGCTGCCA TCCGCAACTA TGGCATCGAG CTGGCCGTGA **GCCTGTGCCA**
GGAGCTTCTG GCCAGTGGCT TGGTGCCAGG CCTCCACTTC TACACCCTCA **ACGCGAGAT**
GGCTACCACA GAGGTGCTGA AGCGCCTGGG GATGTGGACT GAGGACCCCA ^Ggtgagggca
 gtggcccaga gatccccaga ggagggtcca agagcagccc c

EXON 6: 135 bp (bp 1044-1178)

tccctctagc caatcccttg tctcaattct ctgtcccat cctcaccag **GCGTCCCCTA**
CCCTGGGCTC TCAGTGCCCA CCCCAGCGC CGAGAGGAAG ATGTACGTCC **CATCTTCTGG**
GCCTCCAGAC CAAAGAGTTA CATCTACCGT ACCCAGGAGT GGGACGAGTT **CCCTAACGGC**
CGCTG^gtgag ggccctgcaga ccttccttgc aaatacatct ttgttcttgg gagcg

Fig.12A

20/24

EXON 7: 181 bp

(bp 1179-1359)

actgccctct gtcaggagtg tgccctgacc tctgggcacc cctctgccag **GGGCAATTCC**
TCTTCCCCTG CCTTTGGGGA GCTGAAGGAC TACTACCTCT TCTACCTGAA GAGCAAGTCC
CCCAAGGAGG AGCTGCTGAA GATGTGGGGG GAGGAGCTGA CCAGTGAAGC AAGTGTCTTT
GAAGTCTTTG TTCTTTACCT CTCGGGAGAA CCAAACCGGA ATGGTCACAA Agtgagtgat
gctggaagtg gggaccctgg ttcatccct gccctggcc t

EXON 8: 183 bp

(bp 1360-1542)

cagggtgcca aacctgatgg tgcctccagc cagctcaccg tctctcccag **GTGACTTGCC**
TGCCCTGGAA CGATGAGCCC CTGGCGGCTG AGACCAGCCT GCTGAAGGAG GAGCTGCTGC
GGGTGAACCG CCAGGGCATC CTCACCATCA ACTCACAGCC CAACATCAAC GGGAAAGCCGT
CCTCCGACCC CATCGTGGGC TGGGGCCCCA GCGGGGGCTA TGTCTTCCAG AAGgtgtggt
agggaggcac ggggtgcccc cctctcttga ccggcaccgg tgg

EXON 9: 102 bp

(bp 1543-1644)

gggcgtcttg cagggctggg gttggtgaca ggcacctgtc tctcccacag **GCCTACTTAG**
AGTTTTTCAC TTCCCGCGAG ACAGCGGAAG CACTTCTGCA AGTGCTGAAG AAGTACGAGC
TCCGGGTAA TTACCACCTT GTCAATGTGA AGgtaggcca ggccccacgg tccccacaga
gtaccaggcc cttcggtgaa ca

EXON 10: 120 bp

(bp 1645-1764)

actccagttg ttcttgcccc aggtcttacc cccacccac atcccctcag **GGTGAAAACA**
TCACCAATGC CCCTGAACTG CAGCCGAATG CTGTCACTTG GGGCATCTTC CCTGGGCGAG
AGATCATCCA GCCCACCATA GTGGATCCCG TCAGCTTCAT GTTCTGGAAG gtaaaggagc
gggggcaagc ttgccccgcc cacctggaaa accgtgggga

EXON 11: 219 bp (stop codon) (bp 1765-1983)

432 bp (end of cDNA) (bp 1765-2196)

ctctgtgtgt gtgtgcatgt gtgcgtgtgt gcgggggtat gtgtgtgtag **GACGAGGCCT**
TTGCCCTGTG GATTGAGCGG TGGGGAAAGC TGTATGAGGA GGAGTCCCCG TCCCGCACCA
TCATCCAGTA CATCCACGAC AACTACTTCC TGGTCAACCT GGTGGACAAT GACTTCCAC
TGGACAACCTG CCTCTGGCAG GTGGTGGGAAG ACACATTGGA GCTTCTCAAC AGGCCCACCC
AGAATGCGAG AGAAACGGAG GCTCCATGAC CCTGCGTCCT GACGCCCTGC GTTGGAGCCA
CTCCTGTCCC GCCTTCCTCC TCCACAGTGC TGCTTCTCTT GGGAACTCCA CTCTCCTTCG
TGTCTCTCCC ACCCGGCCT CCACTCCCCC ACCTGACAAT GGCAGCTAGA CTGGAGTGAG
GCTTCCAGGC TCTTCCTGGA CCTGAGTCGG CCCACATGG GAACCTAGTA CTCTCTGCTC
TAgccaggag tctgtgctct tttggtgggg agcacttgct cctgcagagg ac

Fig.12B

EXON 1: 243 bp (bp 3-245) 21/24

gggttttggtta ccagccctat aatacccccg gccccccaccc tctacagcag **GAATCCAGCC**
ATGGTGAACG AGGCCAGAGG AAGTGGCAGT CCCAACCCGC GATCTGAGGG **CAGCAGCAGT**
GGCAGCGAGA GTTCCAAGGA CAGTTCAAGA TGTTCACACC CCAGCCTGGA **CCCAGAGCGG**
CACGAGAGAC TCCGGGAGAA GATGAGGCGC AGAATGGACT CTGGTGACAA **GTGGTTCTCC**
CTGGAGTTCT TCCCCCCTCG AACTGCTGAG GGAGCTGTTA **ACCTCATCTC** CAGgtgagta
 gggaggttaa tccgcggggg tcggcaggct tcaggggagc gtg

EXON 2: 239 bp (bp 246-484)

gagctcccta tttaccccag gagcctactt aaggaggaaa tcccctacag **GTTTGACCGG**
ATGGCAGCAG GGGGCCCCCT CTTCGTAGAT GTTACCTGGC **ACCCAGCTGG** **AGACCCTGGC**
TCAGACAAGG AGACCTCCTC CATGATGATC GCCAGCACAG **CAGTAACTA** **CTGCGGCTTG**
GAAACCATCC TGCATATGAC CTGCTGCCAG CAGCGCCCCG **AGGAGATCAC** **AGGCCATCTG**
CACAGAGCCA AGCAGCTGGG CCTGAAGAAC **ATAATGGCGC** **TGAGGGGAGg** **tgtggcgcca**
 gcacccctcc tctttggggt cttgctttcc tgaaggctt

EXON 3: 111 bp (bp 485-595)

tctggaggtc aggggacacc cagtgaccat gacctccagc aaccctgcag **ACCCTGTAGG**
TGACCACTGG GAAGCAGAGG AAGGAGGCTT **CAGCTATGCC** **ACAGACCTGG** **TGAAGCACAT**
CCGGACCGAG TTTGCTGACT **ATTTTGACAT** **CTGTGTGGCA** **Ggtaagtga** **gacagagaag**
 ggtcaggatg agaggatagc cagctagtct t

EXON 4: 194 bp (bp 596-789)

gcaggtaggt tgagaccagc cccctacttc ttcttgtctc ctcttggtag **GTTACCCAG**
AGGCCACCCC GATGCAGAGA GCTTCGAGGA **TGACCTGAAG** **CATTTGAAGG** **AGAAGGTATC**
TGCAGGCGCC GACTTCATTA TCACTCAGCT CTTCTTTGAG **GCCAGCACCT** **TCTTCAGCTT**
TGTGAAGGCC TGCACAGAGA TAGGCATCTC **TTGCCCTATC** **CTGCCTGGGA** **TCTTCCCTAT**
TCAGgtgagg ggcttgggag gacctgattc cctccgtcca gtgcatgcgg aagt

EXON 5: 251 bp (bp 790-1040)

cagtggagca taggccagag atgaccccat gccccttggt tctctgacag **GGCTACACTT**
CCCTTCGGCA GCTTGTAATA CTGTCCAAGC TGGAGGTGCC **ACAGAAGATC** **AAGGATGTAA**
TTGAGCCCAT CAAAGACAAC GATGCTGCCA TCCGCAACTA **CGGCATTGAG** **CTGGCTGTAA**
GGCTGTGCCG GGAGCTGCTG GACAGTGGCT TGGTGCCAGG **CCTCCACTTC** **TATACCCTCA**
ACCGCGAGGT GGCCACCATG GAGGTGCTAA **AGCAACTGGG** **CATGTGGACC** **GAGGACCCCA**
Ggtgagcgg ggdagctgga ggcataccca tgagtcagag tcgcgcagg t g

EXON 6: 135 bp (bp 1041-1175)

ctagctcagt ctacetaagc ccttgtcttt tccctcttcc ttcctccag **GCGTCCCTTG**
CCCTGGGCTC TCAGTGCGCA TCCAAGCGC CGGGAGGAAG **ATGTCCGTCC** **CATCTTCTGG**
GCCTCCAGAC CAAAGAGCTA CATCTACCGC **ACACAGGACT** **GGGATGAGTT** **TCCTAACGGC**
CGCTGgtgag gagagaagcc aggggggtgtt aggaattgct ggtgcctggg tggaa

Fig.13A

EXON 7: 181 bp (bp 1176-1356)

aataggacaa gatttacaac aaagtgcctt gtcccttata ctccctgccag **GGGTAATTCT**
TCCTCACCAG CCTTTGGGGA GCTGAAAGAC TACTACCTCT TCTACCTGAA AAGCAAGTCC
CCCAGGGAGG AGCTGCTGAA GATGTGGGGC GAGGAGCTCA CCAGCGAAGA GAGTGTCTTT
GAAGTCTTTG AACACTACCT CTCTGGAGAG CCGAATCGCC ATGGCTACAG Agtgagtggg
 gtgaggagga acggcccagc tttgtctcag ccttgg

EXON 8: 183 bp (bp 1357-1539)

cccagtccca gactcagtgc tgccctcgct cagcgcaccc tgccctgcag **GTAACCTGCC**
TGCCCTGGAA CGATGAACCC CTGGCAGCGG AAACCAGCCT GATGAAGGAA GAGCTGCTCC
GCGTGAACAG GCTGGGCATC CTCACCATCA ACTCTCAGCC CAACATCAAC GCAAAACCAT
CCTCAGACCC TGTGTGGGGC TGGGGCCCCA GTGGGGGTTA TGTCTTCCAG AAGgtatgct
 aggatgcagt actctcgata tccccagga ctgacacaga acc

EXON 9: 102 bp (bp 1540-1641)

gagaacttgg caagtagtgg ggttgacatg ttgggtgtat tctccctcag **GCCTACCTCG**
AATTCCTCAC CTCCCGTGAA ACTGTGGAGG CGCTTCTGCA GGTGCTGAAG ACATACGAGC
TGCGGGTCAA CTACCACATC GTGGACGTGA AGgtaagcca gctccctccg gcttagacgc
 agcaaggctt gaaaacacct aca

EXON 10: 120 bp (bp 1642-1761)

agcagtggga ggttgcggtc accctgcctc agccctgcct ctgtttctcag **GGAGAGAACA**
TACTAATGC CCCTGAGCTG CAGCCCAATG CCGTGACGTG GGGCATCTTC CCGGGTCGAG
AGATCATCCA GCCTACTGTG GTGGACCCA TCAGCTTCAT GTTCTGGAAG gtaagggagt
 gggagggagt ggaggaccct ggctaccgtg agagcccag

EXON 11: 216 bp (stop codon) (bp 1762-1977)

ggaggtacca gccgtgctga ccctgctcgt gtgtctctgt tcacacgtag **GATGAGGCCT**
TTGCCCTGTG GATCGAGCAG TGGGGCAAGC TATACGAGGA GGAGTCGCCA TCCCGCATGA
TCATCCAATA CATCCATGAC AACTATTTCC TGGTCAACCT GGTGGACAAC GAGTTCCCGC
TGGACAGCTG CCTGTGGCAG GTGGTGGAGG ACACGTTTGA GCTGCTCAAC AGGCATCCCA
CGGAGAGAGA GACACAGGCT CCATGAgcct qcatctctca acaggcacac catggagaga
 gagacacagg ctctgtgagc cgtgcatccc tcaacaggca caccacggag agagagacac
 aggctccgtg agcctgcac cgggtatctt cctcacctgg agccctctc cctcatctct
 ctacaca

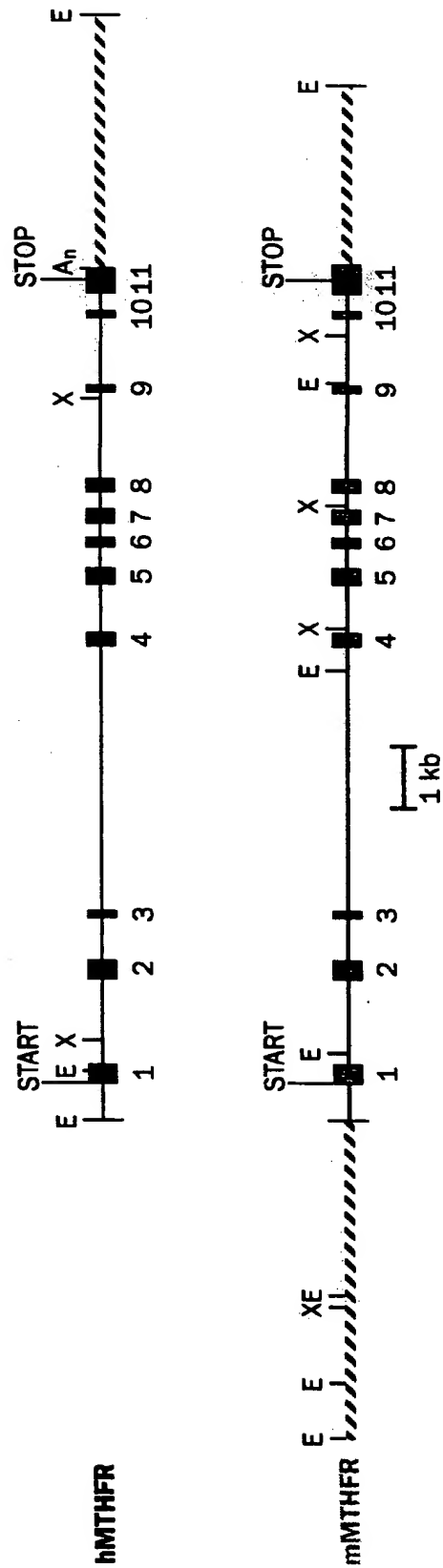


Fig. 14

hMTHFR MVNEARGNSSLNPCLEGSASSGSESSKDSSRCSTPGLDPERHERLREKMRRRLES GDKWF
 mMTHFR 0000000sg0ps0rs000-0000000000000000s0000000000000000mds00000
 bMTHFR -----fhasqrda0nqsl-aevq-0qinv

hMTHFR SLEFFPPRTAEGAVNLISRFDMAAGGPLYIDVTWHPAGDPGSDKETSSMMIASTAVNYC
 mMTHFR 0000000000000000000000000000fv0000000000000000000000000000000
 bMTHFR 0f0000000s0meqt0wnsi00lsslk0kfvs00-yg0-ns0erdr0h0--0kgik-drt

hMTHFR GLETILHMTCCRQRLEEITGHLHKAKQLGLKNIMALRGDPIGDQWEEEEEGGFNYAVDLVK
 mMTHFR 000000d0000q00p00000000r0000000000000000v00h00a00000s00t0000
 bMTHFR 000aap0l00idatpd0lrtiardywnn0irh0v00000lpp-gsgkp0m---00s000t

hMTHFR HIRSEFGDYFDICVAGYPKGHPEAGSFEADLKLKEKVSAGADFIITQLFFEADTFFRFV
 mMTHFR 000t00a00000000000r000d0e000d000000000000000000000000s000s00
 bMTHFR 1lk-0va0-000s00a00ev0000k0aq000ln00r00d000nra000f00dvesyl00r

hMTHFR KACTDMGITCPIVPGIFPIQGYHSLRQLVKLSKLEVPQEIKDVIEPIKDNDAAIRNYGIE
 mMTHFR 0000ei00s000l000000000t000000000000000k0000000000000000000000
 bMTHFR dr0vsa00dve0i000l0vsnfkqakkfadmtnvri0awmaqmf dgl dDaetrklv0an

hMTHFR LAVSLCQELLASGLVPGLHFYTLNREMATTEVLKRLGMWTE DPRRPLPWALSAHPKRREE
 mMTHFR 000x00r000ds000000000000000v00m0000q000000000000000000000000000000
 bMTHFR i0mdmvk-i0sreg0kdf0000000aemsaicht00vr-----

hMTHFR DVRPIFWASRPKSYIYRTQEWDEF PN GRWGNSSSPAFGELKDYYLFY LKSKSPKEELLKM
 mMTHFR 00000000000000000000d000000000000000000000000000000000000000r000000
 bMTHFR -----

hMTHFR WGEELTSEASVFEVFLYLSGEPNRNGHKVTCLPW NDEPLAAETSLLKEELLRVNRQGIL
 mMTHFR 00000000e000000eh00000000h0yr0000000000000000m0000000001000
 bMTHFR -----

hMTHFR TINSQP NINGKPSSDPIVGWGPSGGYVFQKAYLEFFTSRETAEALLQVLKKYELRVNYHL
 mMTHFR 000000000a000000v0000000000000000000000000000v00000000t00000000i
 bMTHFR -----

hMTHFR VNVKGENITNAPELQPN AVTWGIFPGREIIQPTVVDPV SFMFWKDEAFALWIERWGKLYE
 mMTHFR 0d00q000000
 bMTHFR -----

hMTHFR EESPSRTIIQYIHDNYFLVNLVDNDFPLDNCLWQVVEDTLELLNRPTQNARETEAP
 mMTHFR 000000m000000000000000000000e0000s000000000f00000h-pte000q00
 bMTHFR -----

Fig. 15